e) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof;

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences; and

a polypeptide code comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.

REMARKS

Claims 1-5, 8, 11, 13-15, 19, 23-25, 28, 35-37, 39, 47-48, 51 and 57 remain in this application. Claims 6-7, 9-10, 12, 16-18, 20-22, 26-27 29-34, 38, 40-46, 49-50, 52-56 have been canceled. Claims 11, 13, 19, 23, 48, 51 and 57 have been amended.

Attached hereto is a marked-up version of the changes made to the claims by the current Preliminary Amendment. The attached page is captioned "**Version with markings to show changes made**." Also attached is a page showing all the claims as currently pending, which is entitled "**Pending Claims**."

The Commissioner is hereby authorized to credit any overpayment or charge any additional fees in connection with the filing of this Preliminary Amendment to our Deposit Account No. 50-1181.

Respectfully submitted,
GENSET CORPORATION

Date: 13 Apr 01, 2001

By: _____
John Lucas, Ph.D., J.D.
Registration No. 43,373

10665 Sorrento Valley Road
San Diego, CA 92121-1609
Telephone: (858) 597-2600
Facsimile: (858) 597-2601
e-mail: john.lucas@genxy.com

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

11. (Amended) [An isolated, purified, or recombinant polyunucleotide] The polynucleotide of claim 3 consisting essentially of a contiguous span of 8 to 50 nucleotides of anyone of SEQ ID Nos 1 to 3 and 32 to 69 or the complement thereof, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a *G713 or 13q31-q33*-related biallelic marker in said sequence.

13. (Amended) A polynucleotide according to claim [12] 11, wherein said polynucleotide consists essentially of a sequence selected from the following sequences: D1 to D49, and E1 to E49.

19. (Amended) A polynucleotide according to any one of claims 1, 2[, 3, 11, 14, 15 or 16] or 3 attached to a solid support.

23. (Amended) A recombinant vector comprising a polynucleotide according to [any one of claims] claim 1.

37. (Amended) A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:

a) genotyping at least one *G713- or 13q31-q33*-related biallelic marker according to claim [29] 28 for each individual in said population;

b) genotyping a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome of each individual in said population; and

c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

48. (Amended) A method according to [any one of claims 28, 35, 36, 37, 39 or] claim 47 wherein said *13q31-q33*-related biallelic marker is selected from the group consisting of A12 to A49 and the complements thereof.

51. (Amended) A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) [a contiguous span of at least 12 nucleotides of SEQ ID Nos 1, 2 or 3, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions:

1 to 3236, 3547 to 3585 and 4649 to 5222 of SEQ ID No 1, or a variant thereof or a sequence complementary thereto;

1 to 16155 and 16331 to 21278 of SEQ ID No 2 or a variant thereof or a sequence complementary thereto; and

1 to 5531, 6844 to 7237, 7798 to 8184, 8667 to 9074, and 9356 to 21636 of SEQ ID No 3, or a variant thereof or a sequence complementary thereto;] the polynucleotide of claim 1;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

d) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

e) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof; and

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences.

57. (Amended) A method for comparing a first sequence to a reference sequence, comprising the steps of:

reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

a) [a contiguous span of at least 12 nucleotides of SEQ ID Nos 1, 2 or 3, or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions:

1 to 3236, 3547 to 3585 and 4649 to 5222 of SEQ ID No 1, or a variant thereof or a sequence complementary thereto;

1 to 16155 and 16331 to 21278 of SEQ ID No 2 or a variant thereof or a sequence complementary thereto; and

1 to 5531, 6844 to 7237, 7798 to 8184, 8667 to 9074, and 9356 to 21636 of SEQ ID No 3, or a variant thereof or a sequence complementary thereto;] the polynucleotide of claim 1;

b) a contiguous span of at least 12 nucleotides of SEQ ID No 31 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 480 and 717 to 983 of SEQ ID No 31;

c) a contiguous span of at least 12 nucleotides of SEQ ID No 4 or the complements thereof, wherein said contiguous span comprises at least one of the following nucleotide positions: 1 to 519 and 2563 to 5566 of SEQ ID No 4;

f) a contiguous span of at least 12 nucleotides of SEQ ID No 6 or the complements thereof;

g) a contiguous span of at least 12 nucleotides of at least one of SEQ ID Nos 32 to 69, or the complements thereof;

f) a nucleotide sequence complementary to any one of the preceding nucleotide sequences; and

a polypeptide code comprising a contiguous span of at least 6 amino acids of SEQ ID Nos 5 or 7.